

#3
Patent Application US/07/800,3641 SEQUENCE LISTING
2
3
4 (1) GENERAL INFORMATION:
5
6 (i) APPLICANT: Hewick, Rodney M.
7 Wang, Jack H.
8 Wozney, John M.
9 Celeste, Anthony J.
10
11 (ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
12
13 (iii) NUMBER OF SEQUENCES: 12
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
17 (B) STREET: 87 CambridgePark Drive
18 (C) CITY: Cambridge
19 (D) STATE: MA
20 (E) COUNTRY: USA
21 (F) ZIP: 02140
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Kapinos, Ellen J.
36 (B) REGISTRATION NUMBER: 32,245
37 (C) REFERENCE/DOCKET NUMBER: GI 5182A
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 617-876-1170
41 (B) TELEFAX: 617-876-5851
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:
47 (A) LENGTH: 23 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: unknown
51
52 (ii) MOLECULE TYPE: peptide
53

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54 (iii) HYPOTHETICAL: NO
55
56 (iv) ANTI-SENSE: NO
57
58 (vi) ORIGINAL SOURCE:
59 (F) TISSUE TYPE: Bone
60
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp
65 1 5 10 15
66
67 Val Ile Ala Pro Gln Gly Tyr
68 20
69
70 (2) INFORMATION FOR SEQ ID NO:2:
71
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 18 amino acids
74 (B) TYPE: amino acid
75 (C) STRANDEDNESS: single
76 (D) TOPOLOGY: unknown
77
78 (ii) MOLECULE TYPE: peptide
79
80 (iii) HYPOTHETICAL: NO
81
82 (iv) ANTI-SENSE: NO
83
84 (v) FRAGMENT TYPE: internal
85
86 (vi) ORIGINAL SOURCE:
87 (A) ORGANISM: Bos taurus
88 (F) TISSUE TYPE: Bone
89
90
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
92
93 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
94 1 5 10 15
95
96 Leu Arg
97
98
99 (2) INFORMATION FOR SEQ ID NO:3:
100
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 7 amino acids
103 (B) TYPE: amino acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: unknown
106

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107 (ii) MOLECULE TYPE: peptide
108
109 (iii) HYPOTHETICAL: NO
110
111 (iv) ANTI-SENSE: NO
112
113 (vi) ORIGINAL SOURCE:
114 (A) ORGANISM: Bos taurus
115 (F) TISSUE TYPE: Bone
116
117
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
119
120 Ala Cys Cys Ala Pro Thr Lys
121 1 5
122
123 (2) INFORMATION FOR SEQ ID NO:4:
124
125 (i) SEQUENCE CHARACTERISTICS:
126 (A) LENGTH: 23 amino acids
127 (B) TYPE: amino acid
128 (C) STRANDEDNESS: single
129 (D) TOPOLOGY: unknown
130
131 (ii) MOLECULE TYPE: peptide
132
133 (iii) HYPOTHETICAL: NO
134
135 (vi) ORIGINAL SOURCE:
136 (A) ORGANISM: Bos taurus
137 (F) TISSUE TYPE: Bone
138
139
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
141
142 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp
143 1 5 10 15
144
145 Val His Gly Ser His Gly Arg
146 20
147
148 (2) INFORMATION FOR SEQ ID NO:5:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 80 base pairs
152 (B) TYPE: nucleic acid
153 (C) STRANDEDNESS: double
154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: DNA (genomic)
157
158 (iii) HYPOTHETICAL: NO
159

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160 (iv) ANTI-SENSE: NO
161
162 (vi) ORIGINAL SOURCE:
163 (A) ORGANISM: Bos taurus
164
165 (vii) IMMEDIATE SOURCE:
166 (B) CLONE: acc30
167
168 (viii) POSITION IN GENOME:
169 (C) UNITS: bp
170
171 (ix) FEATURE:
172 (A) NAME/KEY: CDS
173 (B) LOCATION: 25..57
174
175
176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
177

178 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51
179 Lys Leu Ser Ala Thr Ser Val Leu Tyr
180 1 5

181
182 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80
183 Tyr Asp
184 10
185
186

187 (2) INFORMATION FOR SEQ ID NO:6:

188
189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 11 amino acids
191 (B) TYPE: amino acid
192 (D) TOPOLOGY: linear
193

194 (ii) MOLECULE TYPE: protein
195

196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
197

198 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
199 1 5 10
200

201 (2) INFORMATION FOR SEQ ID NO:7:

202
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 199 base pairs
205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: double
207 (D) TOPOLOGY: linear
208

209 (ii) MOLECULE TYPE: DNA (genomic)
210

211 (iii) HYPOTHETICAL: NO
212

213 (vi) ORIGINAL SOURCE:
214 (A) ORGANISM: Bos Taurus
215
216 (vii) IMMEDIATE SOURCE:
217 (A) LIBRARY: Bovine genomic
218 (B) CLONE: Lambda 9800-10
219
220 (viii) POSITION IN GENOME:
221 (C) UNITS: bp
222
223 (ix) FEATURE:
224 (A) NAME/KEY: exon
225 (B) LOCATION: 30..199
226
227 (ix) FEATURE:
228 (A) NAME/KEY: intron
229 (B) LOCATION: 1..29
230
231 (ix) FEATURE:
232 (A) NAME/KEY: CDS
233 (B) LOCATION: 30..179
234
235
236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
237
238 TGCCCGCTGC CCCCTCCCGC CCCCGCCAG GTG CAC CTG CTG AAG CCG CAC GCG 533
239 Val His Leu Leu Lys Pro His Ala
240 1 5
241
242 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 1011
243 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
244 10 15 20
245
246 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 1499
247 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
248 25 30 35 40
249
250 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCA ACTCCACCGG 1966
251 Met Val Val Arg Ala Cys Gly Cys His
252 45 50
253
254 CAG 1999
255
256
257 (2) INFORMATION FOR SEQ ID NO:8:
258
259 (i) SEQUENCE CHARACTERISTICS:
260 (A) LENGTH: 49 amino acids
261 (B) TYPE: amino acid
262 (D) TOPOLOGY: linear
263
264 (ii) MOLECULE TYPE: protein
265

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266 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
267
268 Val His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro
269 1 5 10 15
270
271 Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn
272 20 25 30
273
274 Val Ile Leu Arg Lys His Arg Asn Met Val Val Arg Ala Cys Gly Cys
275 35 40 45
276
277 His
278
279
280

281 (2) INFORMATION FOR SEQ ID NO:9:
282

283 (i) SEQUENCE CHARACTERISTICS:
284 (A) LENGTH: 172 base pairs
285 (B) TYPE: nucleic acid
286 (C) STRANDEDNESS: double
287 (D) TOPOLOGY: linear
288
289 (ii) MOLECULE TYPE: DNA (genomic)
290
291 (iii) HYPOTHETICAL: NO
292
293 (vi) ORIGINAL SOURCE:
294 (A) ORGANISM: Bos taurus
295
296 (vii) IMMEDIATE SOURCE:
297 (A) LIBRARY: Bovine genomic
298 (B) CLONE: Lambda 9800-10
299
300 (viii) POSITION IN GENOME:
301 (C) UNITS: bp
302
303 (ix) FEATURE:
304 (A) NAME/KEY: exon
305 (B) LOCATION: 51..161
306
307 (ix) FEATURE:
308 (A) NAME/KEY: intron
309 (B) LOCATION: 1..50
310
311 (ix) FEATURE:
312 (A) NAME/KEY: intron
313 (B) LOCATION: 162..172
314
315 (ix) FEATURE:
316 (A) NAME/KEY: CDS
317 (B) LOCATION: 51..161
318

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319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 320
 321
 322 GGGGTGGGAG GGCACGTGGA TGGGACTCAC CTTCTCCAC TACCCCCAG GAC TGG 56
 323 Asp Trp
 324 1
 325
 326 GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAA GGG GAG TGC 104
 327 Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys
 328 5 10 15
 329
 330 TCC TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GCC ATC CTG 152
 331 Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu
 332 20 25 30
 333
 334 CAG TCC CTG GTCAGTACCT C 172
 335 Gln Ser Leu
 336 35
 337
 338
 339 (2) INFORMATION FOR SEQ ID NO:10:
 340
 341 (i) SEQUENCE CHARACTERISTICS:
 342 (A) LENGTH: 37 amino acids
 343 (B) TYPE: amino acid
 344 (D) TOPOLOGY: linear
 345
 346 (ii) MOLECULE TYPE: protein
 347
 348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 349
 350 Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly 852
 351 1 5 10 15
 352
 353 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
 354 20 25 30
 355
 356 Ile Leu Gln Ser Leu
 357 35
 358
 359 (2) INFORMATION FOR SEQ ID NO:11:
 360
 361 (i) SEQUENCE CHARACTERISTICS:
 362 (A) LENGTH: 119 base pairs
 363 (B) TYPE: nucleic acid
 364 (C) STRANDEDNESS: double
 365 (D) TOPOLOGY: linear
 366
 367 (ii) MOLECULE TYPE: DNA (genomic)
 368
 369 (iii) HYPOTHETICAL: NO
 370
 371 (vi) ORIGINAL SOURCE:

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372 (A) ORGANISM: Bos taurus
373
374 (vii) IMMEDIATE SOURCE:
375 (A) LIBRARY: Bovine genous
376 (B) CLONE: Lambda 9800-10
377
378 (viii) POSITION IN GENOME:
379 (C) UNITS: bp
380
381 (ix) FEATURE:
382 (A) NAME/KEY: exon
383 (B) LOCATION: 20..99
384
385 (ix) FEATURE:
386 (A) NAME/KEY: intron
387 (B) LOCATION: 1..19
388
389 (ix) FEATURE:
390 (A) NAME/KEY: intron
391 (B) LOCATION: 100..119
392
393 (ix) FEATURE:
394 (A) NAME/KEY: CDS
395 (B) LOCATION: 22..99
396
397
398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
399

400 CCCTTGCGTG TCCCCGCAGA C GAC GTC CAC GGC TCC CAC GGC CGG CAG GTG 51
401 Asp Val His Gly Ser His Gly Arg Gln Val
402 1 5 10
403
404 TGC CGT CGG CAC GAG CTG TAC GTG AGC TTC CAG GAC CTG GGC TGG CTG 99
405 Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
406 15 20 25
407
408 GTGAGTTCCG ACTCTCCTT 119
409
410
411 (2) INFORMATION FOR SEQ ID NO:12:
412
413 (i) SEQUENCE CHARACTERISTICS:
414 (A) LENGTH: 26 amino acids
415 (B) TYPE: amino acid
416 (D) TOPOLOGY: linear
417
418 (ii) MOLECULE TYPE: protein
419
420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
421
422 Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His Glu Leu 80
423 1 5 10 15
424

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Raw Sequence Listing

12/16/91

12:00:43

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425 Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
426 20 25

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/800,364

DATE: 12/16/91
TIME: 12:00:44

LINE ERROR

ORIGINAL TEXT

30 Wrong application Serial Number

(A) APPLICATION NUMBER: US

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/800,364

DATE: 12/16/91
TIME: 12:00:44

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/800,364

DATE: 12/16/91
TIME: 12:00:44

LINE ORIGINAL TEXT

CORRECTED TEXT

BACKUP/RESTORE TRANSACTION

Transaction Number:

3383

12/16/91

START TIME: 11:49:13

END TIME: 12:01:11

PROCESSING TIME: 0:11:58

Translog Code	:	DOSCOPY
Application Serial Number	:	US/07/800,364
National PCT	:	N
Admendment	:	
Application Class	:	514
Application File Dt.	:	19911126